

GP 8. (Amended.) A variant of a parent fungal cutinase, which variant comprise a substitution of at least one amino acid residue corresponding to one or more of the following substitutions in the cutinase of *Humicola insolens* strain DSM 1800 (*H. insolens* cutinase numbering):^S

- a) S48E +A88H +N91H +R189V
- b) Q1L +L2K +G8D +N15D
- c) N44D +A130V
- d) Q1C +L2V +G120D
- e) A88L +R189A
- f) S48E +L66I +A88L +I169A +R189H
- g) A88V +S116K +S119P +Q139R +I169V +R189V
- h) A88V +R189A
- i) S48K +A88H +I169G +R189H
- j) Q1L +L2Q +A4V +S11T
- k) T164S
- l) L174F
- m) H49Y
- n) Q1L +L2K +G8D +N15D +S48E +A88H +N91H +R189V
- o) Q1L +L2K +G8D +N15D +N44D +A130V
- p) Q1L +L2K +G8D +N15D +S48E +A88H +N91H +A130V +R189V
- q) G8D +N15D +A16T
- r) A130V
- s) Q1C +L2V
- t) G8D +N15D +A16T
- u) G8D +N15D +S48E +A88H +N91H +A130V +R189V
- v) G8D +N15D +T29M +S48E +A88H +N91H +A130V +R189V
- w) G8D +N15D +T29I +S48E +A88H +N91H +A130V +R189V and/or
- x) G8D +N15D +T29C +S48E +A88H +N91H +A130V +R189V
- y) G8D +N15D +S48E +A88H +N91H +A130V +L174F +I178V +R189V
- z) G8D +N15D +S48E +A88H +N91H +A130V +T166M +I168F +R189V
- aa) G8D +N15D +S48E +A88H +N91H +A130V +T166I +L167P +R189V
- bb) G8D +N15D +V38H +S48E +A88H +N91H +A130V +I169T +R189V

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cc) G8D +N15D +V38H +S48E +A88H +N91H +A130V +R189V

dd) G8D +N15D +T29M +S48E +A88H +N91H +A130V +T166I +L167P +R189V

9. (Amended.) The variant of claim 1, which further comprises at least one amino acid substitution at positions corresponding to Q1, L2, E6, E10, S11, A14, N15, F24, L46, E47, R51, D63, L138 and/or E179 (*H. insolens* cutinase numbering).

10. (Amended.) The variant of claim 1, further comprising at least one substitution corresponding to Q1P, L2V, E6Q, E10Q, S11C, A14P, N15T, F24Y, L46I, E47K, R51P, D63N, L138I and/or E179Q (*H. insolens* cutinase numbering).

11. (Amended.) The variant of claim 1, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q.

12. (Amended.) The variant of claim 1, which has hydrolytic activity towards terephthalic acid esters, particularly towards cyclic tri(ethylene terephthalate) and/or Terephthalic acid bis(2-hydroxyethyl)ester dibenzoate (BETEB).

13. (Amended.) The variant of claim 1, which has a denaturation temperature which is at least 5° higher than the parent cutinase, particularly measured at pH 8.5.

14. (Amended.) A DNA sequence encoding the variant of claim 1.

Concluded 15. (Amended.) A vector comprising the DNA sequence of claim 14.

a3 17. (Amended.) A method of producing the variant of claim 1 or 3, comprising:

- a) cultivating a cell comprising a DNA sequence encoding the variant of claim 1 or 3 so as to express and optionally secrete the variant, and
- b) recovering the variant.

22. (Amended.) The method of claim 18, wherein the parent cutinase:

- a) is native to a filamentous fungus,

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- b) has an amino acid sequence which can be aligned with the cutinase of *H. insolens* strain DSM 1800, or
- c) has an amino acid sequence which is at least 50 % homologous to the cutinase of *H. insolens* strain DSM 1800.

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